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## SEQUENCE LISTING

<110> Kovics, Imre  
Kessler, Paul

<120> VEGF FUSION PROTEINS

<130> 205654

<140> US 09/832,355

<141> 2001-04-10

<160> 126

<170> PatentIn version 3.0

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35 40 45

Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu  
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Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe  
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Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro  
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Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr  
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Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser  
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Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu  
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Lys	Asp	Lys	Asp	Asn	Asp	Asn	Cys	Leu	Asp	Lys	Cys	Ala	Gln	Leu	Arg
				145			150			155			160		

Lys	Gly	Gly	Tyr	Trp	Tyr	Asn	Cys	Cys	Thr	Asp	Ser	Asn	Leu	Asn	Gly
				165				170					175		

Val	Tyr	Tyr	Arg	Leu	Gly	Glu	His	Asn	Lys	His	Leu	Asp	Gly	Ile	Thr
				180				185				190			

Trp	Tyr	Gly	Trp	His	Gly	Ser	Thr	Tyr	Ser	Leu	Lys	Arg	Val	Glu	Met
				195				200				205			

Lys	Ile	Arg	Pro	Glu	Asp	Phe	Lys	Pro							
				210			215								

&lt;210&gt; 24

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

Lys	Pro	Val	Gly	Pro	Trp	Gln	Asp	Cys	Ala	Glu	Ala	Arg	Gln	Ala	Gly
1					5				10			15			

His	Glu	Gln	Ser	Gly	Val	Tyr	Glu	Leu	Arg	Val	Gly	Arg	His	Val	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20

25

30

Ser Val Trp Cys Glu Gln Gln Leu Glu Gly Gly Trp Thr Val Ile  
 35 40 45

Gln Arg Arg Gln Asp Gly Ser Val Asn Phe Phe Thr Thr Trp Gln His  
 50 55 60

Tyr Lys Ala Gly Phe Gly Arg Pro Asp Gly Glu Tyr Trp Leu Gly Leu  
 65 70 75 80

Glu Pro Val Tyr Gln Leu Thr Ser Arg Gly Asp His Glu Leu Leu Val  
 85 90 95

Leu Leu Glu Asp Trp Gly Gly Arg Gly Ala Arg Ala His Tyr Asp Gly  
 100 105 110

Phe Ser Leu Glu Pro Glu Ser Asp His Tyr Arg Leu Arg Leu Gly Gln  
 115 120 125

Tyr His Gly Asp Ala Gly Asp Ser Leu Ser Trp His Asn Asp Lys Pro  
 130 135 140

Phe Ser Thr Val Asp Arg Asp Arg Asp Ser Tyr Ser Gly Asn Cys Ala  
 145 150 155 160

Leu Tyr Gln Arg Gly Gly Trp Trp Tyr His Ala Cys Ala His Ser Asn  
 165 170 175

Leu Asn Gly Val Trp His His Gly His Tyr Arg Ser Arg Tyr Gln  
 180 185 190

Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ala Tyr Ser Leu Arg  
 195 200 205

Lys Ala Ala Met Leu Ile Arg Pro Leu Lys Leu  
 210 215

<210> 25

<211> 215

<212> PRT

<213> Homo sapiens

<400> 25

Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser  
 1 5 10 15

Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn  
 20 25 30

Cys Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His  
 35 40 45

Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly  
 50 55 60

Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His  
 65 70 75 80

Ser Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp  
 85 90 95

Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly  
 100 105 110

Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln  
 115 120 125

Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser  
 130 135 140

Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys  
 145 150 155 160

Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu  
 165 170 175

Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys  
 180 185 190

Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln  
 195 200 205

Ala Thr Thr Met Leu Ile Gln  
 210 215

<210> 26

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Source not known

<400> 26

Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly  
 1 5 10 15

Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys  
 20 25 30

Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp  
 35 40 45

Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe  
 50 55 60

Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser  
 65 70 75 80

Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp  
 85 90 95

Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu

100

105

110

Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu  
 115 120 125

Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr  
 130 135 140

Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser  
 145 150 155 160

Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn  
 165 170 175

Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys Lys  
 180 185 190

Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala  
 195 200 205

Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala Ser  
 210 215 220

<210> 27

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Source not known

<400> 27

His Asp Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu  
 1 5 10 15

His Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe  
 20 25 30

His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln  
 35 40 45

His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr  
 50 55 60

Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu  
 65 70 75 80

Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu  
 85 90 95

Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr  
 100 105 110

Leu Gly Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr  
 115 120 125

Gly Asn Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser  
 130 135 140

Thr Trp Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr  
 145 150 155 160

Ser Gly Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn  
 165 170 175

Gly Lys Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg  
 180 185 190

Gly Leu Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser  
 195 200 205

Thr Lys Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu  
 210 215 220

<210> 28

<211> 214

<212> PRT

<213> Mus musculus

<400> 28

Arg Asp Cys Gln Glu Leu Phe Gln Glu Gly Glu Arg His Ser Gly Leu  
 1 5 10 15

Phe Gln Ile Gln Pro Leu Gly Ser Pro Pro Phe Leu Val Asn Cys Glu  
 20 25 30

Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg Leu Asn Gly  
 35 40 45

Ser Val Asp Phe Asn Gln Ser Trp Glu Ala Tyr Lys Asp Gly Phe Gly  
 50 55 60

Asp Pro Gln Gly Glu Phe Trp Leu Gly Leu Glu Lys Met His Ser Ile  
 65 70 75 80

Thr Gly Asn Arg Gly Ser Gln Leu Ala Val Gln Leu Gln Asp Trp Asp  
 85 90 95

Gly Asn Ala Lys Leu Leu Gln Phe Pro Ile His Leu Gly Gly Glu Asp  
 100 105 110

Thr Ala Tyr Ser Leu Gln Leu Thr Glu Pro Thr Ala Asn Glu Leu Gly  
 115 120 125

Ala Thr Asn Val Ser Pro Asn Gly Leu Ser Leu Pro Phe Ser Thr Trp  
 130 135 140

Asp Gln Asp His Asp Leu Arg Gly Asp Leu Asn Cys Ala Lys Ser Leu  
 145 150 155 160

Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly  
 165 170 175

Gln Tyr Phe His Ser Ile Pro Arg Gln Arg Gln Glu Arg Lys Lys Gly

180

185

190

Ile Phe Trp Lys Thr Trp Lys Gly Arg Tyr Tyr Pro Leu Gln Ala Thr  
 195 200 205

Thr Leu Leu Ile Gln Pro  
 210

<210> 29  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

<400> 29

Phe Gln Asp Cys Ala Glu Ile Lys Arg Ser Gly Val Asn Thr Ser Gly  
 1 5 10 15

Val Tyr Thr Ile Tyr Glu Thr Asn Met Thr Lys Pro Leu Lys Val Phe  
 20 25 30

Cys Asp Met Glu Thr Asp Gly Gly Trp Thr Leu Ile Gln His Arg  
 35 40 45

Glu Asp Gly Ser Val Asn Phe Gln Arg Thr Trp Glu Glu Tyr Lys Glu  
 50 55 60

Gly Phe Gly Asn Val Ala Arg Glu His Trp Leu Gly Asn Glu Ala Val  
 65 70 75 80

His Arg Leu Thr Ser Arg Thr Ala Tyr Leu Leu Arg Val Glu Leu His  
 85 90 95

Asp Trp Glu Gly Arg Gln Thr Ser Ile Gln Tyr Glu Asn Phe Gln Leu  
 100 105 110

Gly Ser Glu Arg Gln Arg Tyr Ser Leu Ser Val Asn Asp Ser Ser Ser  
 115 120 125

Ser Ala Gly Arg Lys Asn Ser Leu Ala Pro Gln Gly Thr Lys Phe Ser  
 130 135 140

Thr Lys Asp Met Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Gln Met  
 145 150 155 160

Leu Ser Gly Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn  
 165 170 175

Gly Ile Tyr Tyr Ser Val His Gln His Leu His Lys Ile Asn Gly Ile  
 180 185 190

Arg Trp His Tyr Phe Arg Gly Pro Ser Tyr Ser Leu His Gly Thr Arg  
 195 200 205

Met Met Leu Arg Pro Met Gly Ala  
 210 215

<210> 30  
 <211> 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Phe	Gln	Asp	Cys	Ala	Glu	Ile	Gln	Arg	Ser	Gly	Ala	Ser	Ala	Ser	Gly
1						5			10					15	

Val	Tyr	Thr	Ile	Gln	Val	Ser	Asn	Ala	Thr	Lys	Pro	Arg	Lys	Val	Phe
							20		25				30		

Cys	Asp	Leu	Gln	Ser	Ser	Gly	Gly	Arg	Trp	Thr	Leu	Ile	Gln	Arg	Arg
						35		40				45			

Glu	Asn	Gly	Thr	Val	Asn	Phe	Gln	Arg	Asn	Trp	Lys	Asp	Tyr	Lys	Gln
						50		55			60				

Gly	Phe	Gly	Asp	Pro	Ala	Gly	Glu	His	Trp	Leu	Gly	Asn	Glu	Val	Val
						65		70		75			80		

His	Gln	Leu	Thr	Arg	Arg	Ala	Ala	Tyr	Ser	Leu	Arg	Val	Glu	Leu	Gln
						85			90			95			

Asp	Trp	Glu	Gly	His	Glu	Ala	Tyr	Ala	Gln	Tyr	Glu	His	Phe	His	Leu
						100			105			110			

Gly	Ser	Glu	Asn	Gln	Leu	Tyr	Arg	Leu	Ser	Val	Val	Gly	Tyr	Ser	Gly
						115		120			125				

Ser	Ala	Gly	Arg	Gln	Ser	Ser	Leu	Val	Leu	Gln	Asn	Thr	Ser	Phe	Ser
						130		135			140				

Thr	Leu	Asp	Ser	Asp	Asn	Asp	His	Cys	Leu	Cys	Lys	Cys	Ala	Gln	Val
						145		150			155			160	

Met	Ser	Gly	Trp	Trp	Phe	Asp	Ala	Cys	Gly	Leu	Ser	Asn	Leu	Asn	
						165			170			175			

Gly	Val	Tyr	Tyr	His	Ala	Pro	Asp	Asn	Lys	Tyr	Lys	Met	Asp	Gly	Ile
						180			185			190			

Arg	Trp	His	Tyr	Phe	Lys	Gly	Pro	Ser	Tyr	Ser	Leu	Arg	Ala	Ser	Arg
						195		200			205				

Met	Met	Ile	Arg	Pro	Leu	Asp	Ile								
						210		215							

&lt;210&gt; 31

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

Lys	Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly
1						5			10			15			

His	Asp	Thr	Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn	Arg
						20			25			30			

Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr  
 35 40 45

Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp  
 50 55 60

Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu  
 65 70 75 80

Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu  
 85 90 95

Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr  
 100 105 110

Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu  
 115 120 125

Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly  
 130 135 140

Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn  
 145 150 155 160

Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His  
 165 170 175

Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg  
 180 185 190

Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser  
 195 200 205

Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His  
 210 215 220

<210> 32

<211> 220

<212> PRT

<213> Homo sapiens

<400> 32

Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu Ala Gly  
 1 5 10 15

His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn Ser Asn Gly  
 20 25 30

Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly Gly Trp Thr  
 35 40 45

Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe Arg Asn Trp  
 50 55 60

Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu  
 65 70 75 80

Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn Tyr Lys Leu  
 85 90 95

Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr Ala Glu Tyr  
 100 105 110

Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg Leu Arg Leu  
 115 120 125

Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp His Asn Gly  
 130 135 140

Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn  
 145 150 155 160

Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His  
 165 170 175

Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys  
 180 185 190

His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Ser Tyr Ser  
 195 200 205

Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
 210 215 220

<210> 33

<211> 136

<212> PRT

<213> Homo sapiens

<400> 33

Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
 1 5 10 15

Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu  
 20 25 30

Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met  
 35 40 45

Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly  
 50 55 60

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
 65 70 75 80

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 85 90 95

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 100 105 110

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Glu Gly  
 115 120 125

Lys Lys Gln Glu Lys Met Leu Asp

130 135

<210> 34  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 34

Lys Lys Lys Asp Lys Val Lys Lys Gly Gly Pro Gly Ser Glu Cys Ala  
 1 5 10 15

Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser Ser Lys Asp Cys Gly Val  
 20 25 30

Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln Thr Gln Arg Ile Arg Cys  
 35 40 45

Arg Val Pro Cys Asn Trp Lys Lys Glu Phe Gly Ala Asp Cys Lys Tyr  
 50 55 60

Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr Lys Val  
 65 70 75 80

Arg Gln Gly Thr Leu Lys Ala Arg Tyr Asn Ala Gln Cys Gln Glu  
 85 90 95

Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr Lys Ala Lys Ala  
 100 105 110

Lys Ala Lys Lys Gly Lys Gly Lys Asp  
 115 120

<210> 35  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 35

Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn Thr Ala  
 1 5 10 15

Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn Ala Glu  
 20 25 30

Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys  
 35 40

<210> 36  
 <211> 54  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 36

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
 1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 35 40 45

Thr Lys Pro Lys Pro Gln  
 50

<210> 37

<211> 72

<212> PRT

<213> Homo sapiens

<400> 37

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
 1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 35 40 45

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Glu Gly  
 50 55 60

Lys Lys Gln Glu Lys Met Leu Asp  
 65 70

<210> 38

<211> 80

<212> PRT

<213> Homo sapiens

<400> 38

Cys Gly Glu Trp Thr Trp Gly Pro Cys Ile Pro Asn Ser Lys Asp Cys  
 1 5 10 15

Gly Leu Gly Thr Arg Glu Gly Thr Cys Lys Gln Glu Thr Arg Lys Leu  
 20 25 30

Lys Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly Ala Asp Cys  
 35 40 45

Lys Tyr Lys Phe Glu Ser Trp Gly Glu Cys Asp Ala Asn Thr Gly Leu  
 50 55 60

Lys Thr Arg Ser Gly Thr Leu Lys Lys Ala Leu Tyr Asn Ala Asp Cys  
 65 70 75 80

<210> 39

<211> 21

<212> PRT

<213> Homo sapiens

<400> 39

Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
1 5 10 15

Glu Trp Gln Trp Ser  
20

<210> 40  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 40

Ser Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp  
1 5 10 15

<210> 41  
<211> 61  
<212> PRT  
<213> Homo sapiens

<400> 41

Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr  
1 5 10 15

Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala  
20 25 30

Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr  
35 40 45

Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp  
50 55 60

<210> 42  
<211> 42  
<212> PRT  
<213> Homo sapiens

<400> 42

Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr  
1 5 10 15

Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys  
20 25 30

Gln Glu Thr Ile Arg Val Thr Lys Pro Cys  
35 40

<210> 43  
<211> 32  
<212> PRT  
<213> Homo sapiens

<400> 43

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala  
 1 5 10 15

Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala  
 20 25 30

<210> 44

<211> 20

<212> PRT

<213> Homo sapiens

<400> 44

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala  
 1 5 10 15

Leu Thr Ser Ala  
 20

<210> 45

<211> 139

<212> PRT

<213> Homo sapiens

<400> 45

Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys  
 1 5 10 15

Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp  
 20 25 30

Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala  
 35 40 45

Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr  
 50 55 60

Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn  
 65 70 75 80

Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr  
 85 90 95

Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys  
 100 105 110

Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys  
 115 120 125

Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser  
 130 135

<210> 46

<211> 15

<212> PRT

<213> Homo sapiens

<400> 46

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys  
1 5 10 15

<210> 47  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 47

Lys Lys Asn Gly Ser Cys Lys Arg  
1 5

<210> 48  
<211> 13  
<212> PRT  
<213> Artificial sequence

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Synthetic

<220>  
<221> misc\_feature  
<222> (5)..(5)  
<223> "Xaa" may be between 5 and 7 of any amino acids

<220>  
<221> misc\_feature  
<222> (7)..(9)  
<223> "Xaa" may be any amino acid

<400> 48

Arg Leu Tyr Cys Xaa Leu Xaa Xaa Xaa Pro Asp Gly Arg  
1 5 10

<210> 49  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 49

Ile Ser Ser Lys  
1

<210> 50  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 50

Lys Lys Pro Lys Leu  
1 5

<210> 51  
 <211> 535  
 <212> PRT  
 <213> Homo sapiens

<400> 51

Met Leu Gly Pro Cys Met Leu Leu Leu Leu Leu Leu Gly Leu Arg  
 1 5 10 15

Leu Gln Leu Ser Leu Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp  
 20 25 30

Phe Trp Asn Arg Glu Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu  
 35 40 45

Gln Pro Ala Gln Thr Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp  
 50 55 60

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln  
 65 70 75 80

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe  
 85 90 95

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro  
 100 105 110

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn  
 115 120 125

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn  
 130 135 140

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys  
 145 150 155 160

Ala Gly Lys Ser Val Gly Val Val Thr Thr Arg Val Gln His Ala  
 165 170 175

Ser Pro Ala Gly Thr Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser  
 180 185 190

Asp Ala Asp Val Pro Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile  
 195 200 205

Ala Thr Gln Leu Ile Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly  
 210 215 220

Gly Arg Lys Tyr Met Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro  
 225 230 235 240

Asp Asp Tyr Ser Gln Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val  
 245 250 255

Gln Glu Trp Leu Ala Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg  
 260 265 270

Thr Glu Leu Met Gln Ala Ser Leu Asp Pro Ser Val Thr His Leu Met

275	280	285
Gly Leu Phe Glu Pro Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser		
290	295	300
Thr Leu Asp Pro Ser Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu		
305	310	315
320		
Leu Ser Arg Asn Pro Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg		
325	330	335
Ile Asp His Gly His His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu		
340	345	350
Thr Ile Met Phe Asp Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser		
355	360	365
Glu Glu Asp Thr Leu Ser Leu Val Thr Ala Asp His Ser His Val Phe		
370	375	380
Ser Phe Gly Gly Tyr Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala		
385	390	395
400		
Pro Gly Lys Ala Arg Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly		
405	410	415
Asn Gly Pro Gly Tyr Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr		
420	425	430
Glu Ser Glu Ser Gly Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro		
435	440	445
Leu Asp Glu Glu Thr His Ala Gly Glu Asp Val Ala Val Phe Ala Arg		
450	455	460
Gly Pro Gln Ala His Leu Val His Gly Val Gln Glu Gln Thr Phe Ile		
465	470	475
480		
Ala His Val Met Ala Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys		
485	490	495
Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala His Pro Gly Arg		
500	505	510
Ser Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu		
515	520	525
Leu Glu Thr Ala Thr Ala Pro		
530	535	
<210> 52		
<211> 22		
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Leu Gln Leu Ser Leu Gly  
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<210> 53  
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<213> Homo sapiens

<400> 53

Ala Ala His Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu  
1 5 10 15

Ala Gly Thr Leu Leu Leu Glu Thr Ala Thr Ala Pro  
20 25

<210> 54  
<211> 108  
<212> PRT  
<213> Homo sapiens

<400> 54

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln  
1 5 10 15

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe  
20 25 30

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro  
35 40 45

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn  
50 55 60

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn  
65 70 75 80

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys  
85 90 95

Ala Gly Lys Ser Val Gly Val Val Thr Thr Thr Arg  
100 105

<210> 55  
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<400> 55

Ala Gln Val Pro Asp Ser Ala Xaa Thr Ala Thr Ala Tyr Leu Cys Gly  
1 5 10 15

Val Lys Ala Asn  
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<210> 56  
<211> 86  
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<223> "Xaa" may be any amino acid

<400> 56

Thr Asn Val Ala Lys Asn Xaa Ile Met Phe Leu Gly Asp Gly Met Gly
1 5 10 15

Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Xaa His His
20 25 30

Xaa Xaa Gly Xaa Glu Thr Xaa Leu Xaa Met Asp Xaa Phe Pro Xaa Val
35 40 45

Ala Leu Ser Lys Thr Tyr Asn Xaa Xaa Ala Gln Val Pro Asp Ser Ala
50 55 60

Xaa Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Ala Asn Xaa Xaa Thr
65 70 75 80

Xaa Gly Xaa Ser Ala Ala
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<210> 57
<211> 53
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<400> 57

Glu Asp Thr Leu Thr Xaa Val Thr Ala Asp His Ser His Val Phe Xaa
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Phe Gly Gly Tyr Thr Xaa Arg Gly Asn Ser Ile Phe Gly Leu Ala Pro
20 25 30

Met Xaa Xaa Asp Thr Asp Lys Lys Xaa Xaa Thr Ala Ile Leu Tyr Gly
35 40 45

Asn Gly Pro Gly Tyr
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<210> 58
<211> 22
<212> PRT
<213> Homo sapiens

<400> 58

Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu
1 5 10 15

Glu Thr Ala Thr Ala Pro
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<210> 59
<211> 154
<212> PRT
<213> Homo sapiens

<400> 59

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly

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20

25

30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val  
 130 135 140

Arg Gly Lys Gly Cys Asp Lys Pro Arg Arg  
 145 150

<210> 60

<211> 162

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<223> Synthetic

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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val  
130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Cys Asp Lys Pro  
145 150 155 160

Arg Arg

<210> 61  
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<400> 61

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys Lys  
130 135 140

Cys Asp Lys Pro Arg Arg  
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<210> 62  
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 <223> Synthetic

<400> 62

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys  
 130 135 140

Lys Lys Lys Cys Asp Lys Pro Arg Arg  
 145 150

<210> 63  
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<400> 63

Gly Gly Gly Gly Ser Ser Ser  
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<210> 64  
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<400> 64

Ile Glu Gly Arg  
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<400> 66

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
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<210> 67

<211> 13

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<222> ()..()

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<400> 67

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Lys Glu Phe  
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<210> 68

<211> 26

<212> PRT

<213> Homo sapiens

<400> 68

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Val Leu His His Ala Lys Trp Ser Gln Ala  
 20 25

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<400> 69  
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33

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39

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28

<210> 73

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cctgatgaga tcgagttacat cttcaagcca atgaactttc tgctgtctt ggtgcattgg      180
agccttgctt tgctgctcta cctccaccat gccaagttgt cccagtcctg tgtgcccctg      240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc      300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa      420
aaatgtgaca agccgaggcg ggaggaagag aaaccattta gagactgtgc agatgtatat      480
caagctggtt ttaataaaag tggaatctac actatttata ttaataatat gccagaaccc      540
aaaaaggtgt tttgcaatat ggatgtcaat gggggaggtt ggactgtaat acaacatcg      600
gaagatggaa gtctagattt ccaaagaggc tggaaaggat ataaaatggg ttttggaaat      660
ccctccggtg aatattggct gggaaatgag tttattttg ccattaccag tcagaggcag      720
tacatgctaa gaattgagtt aatggactgg gaagggaaacc gagccttattc acagtatgac      780
agattccaca taggaaatga aaagcaaaac tataggttgt atttaaaagg tcacactggg      840
acagcaggaa aacagagcag cctgatctt cacggtgctg atttcagcac taaagatgt      900
gataatgaca actgtatgtg caaatgtgcc ctcatgttaa caggaggatg gtggtttgat      960
gcttggtggcc cctccaatct aaatggaaatg ttctatactg cgggacaaaaa ccatggaaaa      1020
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<400> 74

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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
 130 135 140

Pro Arg Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr  
 145 150 155 160

Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn  
 165 170 175

Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly  
 180 185 190

Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln  
 195 200 205

Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu  
 210 215 220

Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln  
 225 230 235 240

Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr  
 245 250 255

Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg  
 260 265 270

Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu  
 275 280 285

Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn  
 290 295 300

Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp

305	310	315	320
Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln			
325	330	335	
Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro			
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Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe			
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 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300  
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360  
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420  
 aaatgtgaca agccgaggcg gcaatttggc gcggagtgca aataccagtt ccaggcctgg 480  
 ggagaatgtg acctgaacac agccctgaag accagaactg gaagtctgaa gcgagccctg 540  
 cacaatgccc aatgccagaa gactgtcacc atctccaagc cctgtggcaa actgaccaag 600  
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<400> 79

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
 130 135 140

Pro Arg Arg Gln Phe Gly Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp  
 145 150 155 160

Gly Glu Cys Asp Leu Asn Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu  
 165 170 175

Lys Arg Ala Leu His Asn Ala Glu Cys Gln Lys Thr Val Thr Ile Ser  
 180 185 190

Lys Pro Cys Gly Lys Leu Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys  
 195 200 205

Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp  
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<210> 80

<211> 37

<212> DNA

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<222> ()...()

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<211> 37

<212> DNA

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<400> 81

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<212> DNA

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27



65	70	75	80
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Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro	85	90	95
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Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His	100	105	110
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Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys	115	120	125
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Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys	130	135	140
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Pro Arg Arg Glu Phe Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp	145	150	155	160
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Gly Ala Cys Asp Gly Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu	165	170	175
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Lys Lys Ala Arg Tyr Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr	180	185	190
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Lys Pro Cys Thr Pro Lys Thr Lys Ala Lys Ala Lys Lys Gly	195	200	205
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Lys Gly Lys Asp	210
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<211> 36
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36
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<223> Synthetic
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36
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<210> 87
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aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg	360	
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa	420	
aaatgtgaca agccgaggcg gaagccgtcg ggcctatggc gagactgcct gcaggccctg	480	
gaggatggcc acgacaccag ctccatctac ctggtaagc cggagaacac caaccgcctc	540	
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agtttccggcc tggAACCTGA gagcgagtat tataagctgc ggctggggcg ctaccatggc	840	
aatgcgggtg actccttac atggcacaac ggcaagcagt tcaccaccct ggacagagat	900	
catgatgtct acacaggaaa ctgtgeccac taccagaagg gaggctggtg gtataacgcc	960	
tgtgcccact ccaacctcaa cgggtctgg taccgcgggg gccattaccg gagccgctac	1020	
caggacggag tctactggc tgagttccga ggaggcttt actcactcaa gaaagtggtg	1080	
atgatgatcc gaccgaaccc caacacccccc cactaa	1116	
 <210> 89		

<211> 371  
<212> PRT  
<213> Artificial sequence

<220>  
<221> misc\_feature  
<222> ()...()  
<223> Synthetic

<400> 89

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
130 135 140

Pro Arg Arg Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu  
145 150 155 160

Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn  
165 170 175

Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly  
180 185 190

Gly Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe  
195 200 205

Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu  
210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn  
225 230 235 240

Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe  
245 250 255

Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys  
 260 265 270

Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp  
 275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr  
 290 295 300

Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala  
 305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr  
 325 330 335

Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly  
 340 345 350

Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn  
 355 360 365

Thr Phe His  
 370

<210> 90  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 90  
 gaatggtcct tcattgatcc gcctcggctt gtcaca

36

<210> 91  
 <211> 36  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 91  
 tgtgacaagc cgaggcggat caatgaagga ccattc

36

<210> 92  
 <211> 29  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 92		
cgccggatcct cagtcaatacg gcttgatca		29
<210> 93		
<211> 1104		
<212> DNA		
<213> Artificial sequence		
<220>		
<221> misc_feature		
<222> ()..()		
<223> Synthetic		
<400> 93		
atgaactttc tgctgtcttg ggtgcattgg agccttgccct tgctgctcta cctccaccat	60	
gccaagtggc cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg	120	
gtgaagttca tggatgtctta tcagcgcagc tactgccatc caatcgagac cctgggtggac	180	
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg	240	
atgcgatgct ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc	300	
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg	360	
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa	420	
aaatgtgaca agccgaggcg gatcaatgaa ggaccattca aagactgtca gcaagcaaaa	480	
gaagctgggc attcggtcag tgggatttat atgattaaac ctgaaaacag caatggacca	540	
atgcagttat ggtgtgaaaa cagtttggac cctgggggtt ggactgttat tcagaaaaga	600	
acagacggct ctgtcaactt cttcagaaat tggaaaatt ataagaaagg gtttggaaac	660	
attgacggag aatactggct tggactggaa aatatctata tgcttagcaa tcaagataat	720	
tacaagttat tgattgaatt agaagactgg agtataaaaa aagtctatgc agaatacagc	780	
agcttcgtc tggAACCTGA aagtgaattc tatagactgc gcctggaaac ttaccaggaa	840	
aatgcagggg attctatgat gtggcataat ggtaaacaat tcaccacact ggacagagat	900	
aaagatatgt atgcaggaaa ctgcggccac tttcataaaag gaggctggtg gtacaatgcc	960	
tgtgcacatt ctaacctaaa tggagtatgg tacagaggag gccattacag aagcaagcac	1020	
caagatggaa ttttctggc cgaatacaga ggccgggtcat actccttaag agcagttcag	1080	
atgatgatca agcctattga ctga	1104	
<210> 94		
<211> 367		
<212> PRT		
<213> Artificial sequence		
<220>		

<221> misc\_feature  
 <222> ()..()  
 <223> Synthetic  
 <400> 94

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
 130 135 140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys  
 145 150 155 160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn  
 165 170 175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly  
 180 185 190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe  
 195 200 205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu  
 210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn  
 225 230 235 240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr  
 245 250 255

Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg  
 260 265 270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp  
 275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr  
 290 295 300  
 Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala  
 305 310 315 320  
 Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr  
 325 330 335  
 Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly  
 340 345 350  
 Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
 355 360 365  
  
 <210> 95  
 <211> 1387  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic  
  
 <220>  
 <221> misc\_feature  
 <222> (1201)..(1219)  
 <223> "n" may be any nucleotide  
  
 <220>  
 <221> misc\_feature  
 <222> (1295)..(1324)  
 <223> "n" may be any nucleotide  
  
 <400> 95

atgtggcaga	ttgtttctt	tactctgagc	tgtgatcttg	tcttggccgc	agcctataac	60
aactttcgga	agagcatgga	cagcatagga	aagaagcaat	atcaggtcca	gcatgggtcc	120
tgcagctaca	cttcctcct	gccagagatg	gacaactgcc	gctttccctc	cagccctac	180
gtgtccaaatg	ctgtgcagag	ggacgcgccc	ctcgaatacg	atgactcggt	gcagaggctg	240
caagtgctgg	agaacatcat	ggaaaacaac	actcagtggc	taatgaaggt	agagaatata	300
tcccaggaca	acatgaagaa	agaaatggta	gagatacagc	agaatgcagt	acagaaccag	360
acggctgtga	tgatagaaat	agggacaaac	ctgttgaacc	aaacagcgg	gcaaacgcgg	420
aagtttaactg	atgtggaagc	ccaagtatta	aatcagacca	cgagacttga	acttcagctc	480
tttggAACACT	CCCTCTCGAC	AAACAAATTG	AAAAAACAGA	TTTGGACCA	GACCAGTGA	540
ATAAACAAAT	TGCAAGATAA	GAACAGTTTC	CTAGAAAAGA	AGGTGCTAGC	TATGGAAAGAC	600
AAAGCACATCA	TCCAACCTACA	QTCAATAAAA	QAAGAQAAAG	ATCAQCTACA	GGTGTAGTA	660

tccaaggcaga attccatcat tgaagaactc	gaaaaaaaaaa tagtgactgc	cacggtaat	720
aattcagttc ttcagaagca gcaacatgat	ctcatggaga cagttataa	cttactgact	780
atgatgtcca catcaaacgc	agctaaggac cccactgtt	ctaaagaaga acaaatcagc	840
ttcagagact gtgctgaagt	attcaaatac ggacacacca	cgaatggcat ctacacgtt	900
acattcccta attctacaga agagatcaag	gcctactgt	acatggaagc tggaggaggc	960
gggtggacaa ttattcagcg acgtgaggat	ggcagcg	tttgcagag gacttggaaa	1020
gaatataaag tgggatttgg taacctctca	gaaaaatatt ggctggaaa	tgagttgtt	1080
tcgcaactga ctaatcagca acgctatgt	ctaaaatac accttaaaga	ctgggaaggg	1140
aatgaggctt actcattgta tgaacatttc	tatctctcaa	gtgaagaact caattatagg	1200
nnnnnnnnnn nnnnnnnnnng	gcaatgattt tagcacaagg	gatggagcca	1260
tatttgcaaa tgttcacaaa tgctaacagn	aggtnnnnnn	nnnnnnnnnn nnnnnnnnnn	1320
nnnntactgg aaaggctcag	gctattcgct	caaggccaca accatgatga	1380
agatttc			1387

&lt;210&gt; 96

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; ()..()

&lt;223&gt; Synthetic

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (269)..(272)

&lt;223&gt; "Xaa" may be any amino acid

&lt;400&gt; 96

Met	Trp	Gln	Ile	Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala
1				5				10					15		

Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys
					20			25				30			

Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro
					35			40				45			

Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Pro	Tyr	Val	Ser	Asn	Ala
					50			55				60		

Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val	Gln	Arg	Leu
					65			70				75			80

Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp	Leu	Met	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile  
 100 105 110

Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly  
 115 120 125

Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp  
 130 135 140

Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu Glu Leu Gln Leu  
 145 150 155 160

Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp  
 165 170 175

Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu  
 180 185 190

Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser  
 195 200 205

Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn  
 210 215 220

Ser Ile Ile Glu Glu Leu Glu Lys Ile Val Thr Ala Thr Val Asn  
 225 230 235 240

Asn Ser Val Leu Gln Lys Gln His Asp Leu Met Glu Thr Val Asn  
 245 250 255

Asn Leu Leu Thr Met Met Ser Thr Ser Asn Cys Lys Xaa Xaa Xaa Xaa  
 260 265 270

Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe  
 275 280 285

Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Met Trp Gln Ile  
 290 295 300

Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala Ala Ala Tyr Asn  
 305 310 315 320

Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys Gln Tyr Gln Val  
 325 330 335

Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro Glu Met Asp Asn  
 340 345 350

Cys Arg Ser Ser Ser Pro Tyr  
 355 360

<210> 97

<211> 339

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 97

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
 130 135 140

Pro Arg Arg Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val  
 145 150 155 160

Asn Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu  
 165 170 175

Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro  
 180 185 190

Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser  
 195 200 205

Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn  
 210 215 220

Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln  
 225 230 235 240

Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln  
 245 250 255

Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp  
 260 265 270

Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp  
 275 280 285

Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr  
 290 295 300

Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe  
 305 310 315 320

Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro  
 325 330 335

Leu Asp Phe

<210> 98  
 <211> 361  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 98  
 gtccaatgct gtgcagaggg acgcgcgcgt cgaatacgat gactcggtgc agaggctgca 60  
 agtgctggag aacatcatgg aaaacaacac tcagtggcta atgaaggtag agaatatatc 120  
 ccaggacaac atgaagaaag aaatggtaga gatacagcag aatgcagtac agaaccagac 180  
 ggctgtatg atagaaatag ggacaaacct gttgaaccaa acagcggagc aaacgcggaa 240  
 gttaactgat gtggaagccc aagtattaaa tcagaccacg agacttgaac ttcagcttt 300  
 ggaacactcc ctctcgacaa acaaattgga aaaacagatt ttggaccaga ccagtgaaat 360  
 a 361

<210> 99  
 <211> 123  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 99

Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser  
 1 5 10 15

Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln  
 20 25 30

Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu  
 35 40 45

Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met

50	55	60	
Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg			
65	70	75	80
Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu			
85	90	95	
Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys			
100	105	110	
Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys			
115	120		
<210> 100			
<211> 462			
<212> PRT			
<213> Artificial sequence			
<220>			
<221> misc_feature			
<222> ()..()			
<223> Synthetic			
<400> 100			
Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser			
1	5	10	15
Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln			
20	25	30	
Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu			
35	40	45	
Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met			
50	55	60	
Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg			
65	70	75	80
Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu			
85	90	95	
Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys			
100	105	110	
Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Met Asn Phe Leu Leu			
115	120	125	
Ser Trp Val His Trp Ser Leu Ala Leu Leu Tyr Leu His His Ala			
130	135	140	
Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly Gln Asn His			
145	150	155	160
His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His			
165	170	175	

Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile  
 180 185 190  
 Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly  
 195 200 205  
 Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn  
 210 215 220  
 Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile  
 225 230 235 240  
 Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys  
 245 250 255  
 Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg Arg Met Pro  
 260 265 270  
 Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Trp  
 275 280 285  
 Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly  
 290 295 300  
 Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp  
 305 310 315 320  
 Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met  
 325 330 335  
 Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln  
 340 345 350  
 Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr  
 355 360 365  
 Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu  
 370 375 380  
 His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asn Cys Met  
 385 390 395 400  
 Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys  
 405 410 415  
 Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His  
 420 425 430  
 Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr  
 435 440 445  
 Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe  
 450 455 460  
 <210> 101  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 101

Lys	Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly
1				5					10				15		

His	Asp	Thr	Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn	Arg
				20				25				30			

Leu	Met	Gln	Val	Trp	Cys	Asp	Gln	Arg	His	Asp	Pro	Gly	Gly	Trp	Thr
					35		40				45				

Val	Ile	Gln	Arg	Arg	Leu	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Asn	Trp
				50			55			60					

Glu	Thr	Tyr	Lys	Gln	Gly	Phe	Gly	Asn	Ile	Asp	Gly	Glu	Tyr	Trp	Leu
				65		70			75			80			

Gly	Leu	Glu	Asn	Ile	Tyr	Trp	Leu	Thr	Asn	Gln	Gly	Asn	Tyr	Lys	Leu
				85				90			95				

Leu	Val	Thr	Met	Glu	Asp	Trp	Ser	Gly	Arg	Lys	Val	Phe	Ala	Glu	Tyr
			100				105				110				

Ala	Ser	Phe	Arg	Leu	Glu	Pro	Glu	Ser	Glu	Tyr	Tyr	Lys	Leu	Arg	Leu
			115				120			125					

Gly	Arg	Tyr	His	Gly	Asn	Ala	Gly	Asp	Ser	Phe	Thr	Trp	His	Asn	Gly
			130			135				140					

Lys	Gln	Phe	Thr	Thr	Leu	Asp	Arg	Asp	His	Asp	Val	Tyr	Thr	Gly	Asn
			145			150			155			160			

Cys	Ala	His	Tyr	Gln	Lys	Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His
			165					170			175				

Ser	Asn	Leu	Asn	Gly	Val	Trp	Tyr	Arg	Gly	Gly	His	Tyr	Arg	Ser	Arg
			180				185				190				

Tyr	Gln	Asp	Gly	Val	Tyr	Trp	Ala	Glu	Phe	Arg	Gly	Gly	Ser	Tyr	Ser
			195				200			205					

Leu	Lys	Lys	Val	Val	Met	Met	Ile	Arg	Pro	Asn	Pro	Asn	Thr	Phe	His
			210			215				220					

&lt;210&gt; 102

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

Ile	Asn	Glu	Gly	Pro	Phe	Lys	Asp	Cys	Gln	Gln	Ala	Lys	Glu	Ala	Gly
1				5					10			15			

His	Ser	Val	Ser	Gly	Ile	Tyr	Met	Ile	Lys	Pro	Glu	Asn	Ser	Asn	Gly
			20				25			30					

Pro	Met	Gln	Leu	Trp	Cys	Glu	Asn	Ser	Leu	Asp	Pro	Gly	Gly	Trp	Thr
			35			40				45					

Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe Arg Asn Trp  
 50 55 60

Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu  
 65 70 75 80

Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn Tyr Lys Leu  
 85 90 95

Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr Ala Glu Tyr  
 100 105 110

Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg Leu Arg Leu  
 115 120 125

Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp His Asn Gly  
 130 135 140

Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn  
 145 150 155 160

Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His  
 165 170 175

Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys  
 180 185 190

His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Ser Tyr Ser  
 195 200 205

Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
 210 215 220

<210> 103

<211> 371

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Synthetic

<400> 103

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

65	70	75	80
Met Arg Cys Gly Gly Cys Cys Asn Asp	Glu Gly Leu Glu Cys Val Pro		
85	90	95	
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His			
100	105	110	
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys			
115	120	125	
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys			
130	135	140	
Pro Arg Arg Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu			
145	150	155	160
Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn			
165	170	175	
Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly			
180	185	190	
Gly Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe			
195	200	205	
Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu			
210	215	220	
Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn			
225	230	235	240
Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe			
245	250	255	
Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys			
260	265	270	
Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp			
275	280	285	
His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr			
290	295	300	
Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala			
305	310	315	320
Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr			
325	330	335	
Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly			
340	345	350	
Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn			
355	360	365	
Thr Phe His			
370			

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<210> 104
<211> 367
<212> PRT
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 104

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys
145 150 155 160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
165 170 175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly
180 185 190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe
195 200 205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu
210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn
225 230 235 240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr
245 250 255

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Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg  
260 265 270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp  
275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr  
290 295 300

Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala  
305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr  
325 330 335

Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly  
340 345 350

Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
355 360 365

<210> 105

<211> 53

<212> PRT

<213> Homo sapiens

<400> 105

Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu  
1 5 10 15

Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile  
20 25 30

Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr  
35 40 45

Asp Val Glu Ala Gln  
50

<210> 106

<211> 105

<212> PRT

<213> Homo sapiens

<400> 106

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg  
1 5 10 15

Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly  
20 25 30

Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro  
35 40 45

Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu  
50 55 60

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln  
 65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln  
 85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys  
 100 105

<210> 107

<211> 192

<212> PRT

<213> Homo sapiens

<400> 107

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys  
 1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser  
 20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp  
 35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn  
 50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile  
 65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys  
 85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg  
 100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln  
 115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser  
 130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln  
 145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn  
 165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro  
 180 185 190

<210> 108

<211> 196

<212> PRT

<213> Homo sapiens

<400> 108

Pro Tyr Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp  
 1 5 10 15  
 Asp Ser Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn  
 20 25 30  
 Thr Gln Trp Leu Met Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys  
 35 40 45  
 Lys Glu Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala  
 50 55 60  
 Val Met Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln  
 65 70 75 80  
 Thr Arg Lys Leu Thr Asp Val Glu Ala Gln Val Leu Asn Gln Thr Thr  
 85 90 95  
 Arg Leu Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu  
 100 105 110  
 Glu Lys Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp  
 115 120 125  
 Lys Asn Ser Phe Leu Glu Lys Lys Val Leu Ala Met Glu Asp Lys His  
 130 135 140  
 Ile Ile Gln Leu Gln Ser Ile Lys Glu Glu Lys Asp Gln Leu Gln Val  
 145 150 155 160  
 Leu Val Ser Lys Gln Asn Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile  
 165 170 175  
 Val Thr Ala Thr Val Asn Asn Ser Val Leu Gln Lys Gln Gln His Asp  
 180 185 190  
 Leu Met Glu Thr  
 195  
 <210> 109  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens  
 <400> 109  
 His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg  
 1 5 10 15  
 Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly  
 20 25 30  
 Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro  
 35 40 45  
 Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu  
 50 55 60

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln  
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln  
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys  
100 105

<210> 110

<211> 192

<212> PRT

<213> Homo sapiens

<400> 110

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys  
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser  
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp  
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn  
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile  
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys  
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg  
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln  
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser  
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln  
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn  
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro  
180 185 190

<210> 111

<211> 135

<212> PRT

<213> Homo sapiens

<400> 111

Asp Ala Ser Thr Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn  
1 5 10 15

Leu Lys Asp Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln  
20 25 30

Leu Val Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu  
35 40 45

Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met  
50 55 60

Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu  
65 70 75 80

Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met Leu Lys  
85 90 95

Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr  
100 105 110

Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu Leu Glu Glu Gln  
115 120 125

Cys Leu Arg Ile Phe Ser Arg  
130 135

<210> 112

<211> 101

<212> PRT

<213> Homo sapiens

<400> 112

Glu Leu Glu Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile  
1 5 10 15

Glu Thr Leu Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu  
20 25 30

Val Lys Leu Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr  
35 40 45

Gln Leu Tyr Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn  
50 55 60

Ala Leu Glu Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln Thr Ala  
65 70 75 80

Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu His Lys Tyr  
85 90 95

Gln His Leu Ala Thr  
100

<210> 113

<211> 493

<212> PRT

<213> Homo sapiens

&lt;400&gt; 113

Met Arg Pro Leu Cys Val Thr Cys Trp Trp Leu Gly Leu Leu Ala Ala  
1 5 10 15

Met Gly Ala Val Ala Gly Gln Glu Asp Gly Phe Glu Gly Thr Glu Glu  
20 25 30

Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys Arg Ala Gly  
35 40 45

Glu Ser Gln Asp Lys Gys Thr Tyr Thr Phe Ile Val Pro Gln Gln Arg  
50 55 60

Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu Pro Glu Val Leu Leu  
65 70 75 80

Glu Asn Arg Val His Lys Gln Glu Leu Glu Leu Leu Asn Asn Glu Leu  
85 90 95

Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu Gln Gln Leu Val Glu Val  
100 105 110

Asp Gly Gly Ile Val Ser Glu Val Lys Leu Leu Arg Lys Glu Ser Arg  
115 120 125

Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu  
130 135 140

Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn  
145 150 155 160

Arg Ile Leu Asn Gln Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr  
165 170 175

Lys Asp Leu Glu His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn  
180 185 190

Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro  
195 200 205

Ser Ala Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val  
210 215 220

Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn  
225 230 235 240

Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro  
245 250 255

Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser  
260 265 270

Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly His Asp Thr  
275 280 285

Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg Leu Met Gln  
290 295 300

Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln  
 305 310 315 320

Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr  
 325 330 335

Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu  
 340 345 350

Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr  
 355 360 365

Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe  
 370 375 380

Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr  
 385 390 395 400

His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe  
 405 410 415

Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His  
 420 425 430

Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu  
 435 440 445

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp  
 450 455 460

Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys  
 465 470 475 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His  
 485 490

<210> 114

<211> 54

<212> PRT

<213> Homo sapiens

<400> 114

Thr Asn Lys Leu Glu Arg Gln Met Leu Met Gln Ser Arg Glu Leu Gln  
 1 5 10 15

Arg Leu Gln Gly Arg Asn Arg Ala Leu Glu Thr Arg Leu Gln Ala Leu  
 20 25 30

Glu Ala Gln His Gln Ala Gln Leu Asn Ser Leu Gln Glu Lys Arg Glu  
 35 40 45

Gln Leu His Ser Leu Leu  
 50

<210> 115

<211> 145

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

Thr Gln Gln Val Lys Gln Leu Glu Gln Ala Leu Gln Asn Asn Thr Gln  
1 5 10 15Trp Leu Lys Lys Leu Glu Arg Ala Ile Lys Thr Ile Leu Arg Ser Lys  
20 25 30Leu Glu Gln Val Gln Gln Met Ala Gln Asn Gln Thr Ala Pro Met  
35 40 45Leu Glu Leu Gly Thr Ser Leu Leu Asn Gln Thr Thr Ala Gln Ile Arg  
50 55 60Lys Leu Thr Asp Met Glu Ala Gln Leu Leu Asn Gln Thr Ser Arg Met  
65 70 75 80Asp Ala Gln Met Pro Glu Thr Phe Leu Ser Thr Asn Lys Leu Glu Asn  
85 90 95Gln Leu Leu Leu Gln Arg Gln Lys Leu Gln Gln Leu Gln Gly Gln Asn  
100 105 110Ser Ala Leu Glu Lys Arg Leu Gln Ala Leu Glu Thr Lys Gln Gln Glu  
115 120 125Glu Leu Ala Ser Ile Leu Ser Lys Lys Ala Lys Leu Leu Asn Thr Leu  
130 135 140Ser  
145

&lt;210&gt; 116

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 116  
gcccatggag agactgcctg caggccctgg agatggcca cgacaccagc tccatctacc 60  
tggtaagcc ggagaacacc aaccgcctca tgcaggtgtg gtgcgaccag agacacgacc 120  
ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180  
gggagacgta caagcaaggg tttggaaaca ttgacggcga atactggctg ggcctggaga 240  
acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactgg 300  
ccggccgcaa agtcttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360  
ataagctgcg gctggggcgc taccatggca atgcgggtga ctcccttaca tggcacaacg 420  
gcaaggcagtt caccacccag gacagagatc atgatgtcta cacag 465

&lt;210&gt; 117

&lt;211&gt; 305

&lt;212&gt; DNA

<213> Homo sapiens

<400> 117  
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aattcagagg cgccacgatg gctcagtgga cttcaaccgg ccctkggtag cctacaaggc 120  
ggtggttttggggatcccc acggcgagtt ctggcttggg tcttggagaa aggkgcatag  
catcacgggg ggaccggaac agccgmctgg ccgtgcaamc tgcggggact gggatggca 180  
300  
aacgc 305

<210> 118  
<211> 458  
<212> DNA  
<213> Homo sapiens

<220>  
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<223> "n" may be any nucleotide

<220>  
<221> misc\_feature  
<222> (347)..(347)  
<223> "n" may be any nucleotide

<220>  
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<222> (353)..(353)  
<223> "n" may be any nucleotide

<220>  
<221> misc\_feature  
<222> (384)..(384)  
<223> "n" may be any nucleotide

<220>  
<221> misc\_feature  
<222> (400)..(400)  
<223> "n" may be any nucleotide

<220>  
<221> misc\_feature  
<222> (446)..(446)  
<223> "n" may be any nucleotide

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actaccagaa gggaggctgg tggtataacg cctgtgccc ctcacaccc aaccggggtc 180  
tggtaccgcg gggccatTA ccggagccgc taccaggacg gagngtactg ggctgagttc 240

cgaggaggct	cttactcact	caaggaaacg	tggtgatgat	gatccgaccg	aaccccaaca	300
ccttccacta	agccagctcc	ccctccctgac	ctctccgtgg	ccattgnacag	gangcccacc	360
ctggtcacgc	tggccacagc	acanagaaca	actcctcact	agttcatcct	gaggctggga	420
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<212>	DNA					
<213>	Artificial sequence					
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<222>	()..()					
<223>	Synthetic					
<400>	119					
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<210>	120					
<211>	638					
<212>	DNA					
<213>	Artificial sequence					
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<221>	misc_feature					
<222>	()..()					
<223>	Synthetic					
<400>	120					
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ccgggggctg	gaccgtcatc	cagagacgcc	tggatggctc	tgttaacttc	ttcaggaact	180
gggagacgta	caagcaaggg	tttgggaaca	ttgacggcga	atactggctg	ggcctggaga	240
acatttactg	gctgacgaac	caaggcaact	acaaactcct	ggtgaccatg	gaggactgg	300
ccggccgcaa	agtctttgca	gaatacgcca	gttccgcct	ggaacctgag	agcgagtatt	360
ataagctgcg	gctggggcgc	taccatggca	atgcgggtga	ctccttaca	tggcacaacg	420
gcaagcagtt	caccacccag	gacagagatc	atgatgtcta	cacagtataa	gctgcggctg	480
ggcgataacc	atggcaatgc	gggtgactcc	tttacatggc	acaacggcaa	gcagttcacc	540
accctggaca	gagatcatga	tgtctacaca	ggaaactgtg	cccactacca	gaagggaggc	600
tggtgtata	acgcctgtgc	ccactccaac	ctcaaccg			638
<210>	121					

<211> 4045  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic  
  
 <400> 121  
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 ccggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180  
 gggagacgta caagcaaggg tttgggaaca ttgacggcga atactggctg ggcctggaga 240  
 acatttactg gctgacgaaac caaggcaact acaaactcct ggtgaccatg gaggactgg 300  
 ccggccgcaa agtctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360  
 ataagctgca gctggggcgc taccatggca atgcgggtga ctctttaca tggcacaacg 420  
 gcaagcagtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggctg 480  
 gggcgatacc atggcaatgc gggtaactcc tttacatggc acaacggcaa gcagttcacc 540  
 accctggaca gagatcatga tgtctacaca ggaaactgtg cccactacca gaagggaggc 600  
 tggtgtata acgcctgtgc ccactccaac ctcaaccgga aaaagagagg aagagaaacc 660  
 atttagagac tgtgcagatg tatacaagc tggtttaat aaaagtggaa tctacactat 720  
 ttatattaat aatatgccag aacccaaaaa ggtgtttgc aatatggatg tcaatggggg 780  
 aggttggact gtaatacaac atcgtgaaga tggaaagtcta gatttccaaa gaggctggaa 840  
 ggaatataaa atgggttttgc gaaatccctc cggtaatat tggctggggatgagtttat 900  
 ttttgcatt accagtcaga ggcagtacat gctaagaatt gagttaatgg actggaaagg 960  
 gaaccgagcc tattcacagt atgacagatt ccacatagga aatgaaaagc aaaactatag 1020  
 gttgtattta aaaggtcaca ctgggacagc aggaaaacag agcagcctga tcttacacgg 1080  
 tgctgatttc agcactaaag atgctgataa tgacaactgt atgtgcaaatt gtgcctcat 1140  
 gttaacagga ggtatgggttgc tggatgcttgc tggccctcc aatctaaatg gaatgttcta 1200  
 tactgcggga caaaaaccatg gaaaactgaa tggataaag tggcactact tcaaaggccc 1260  
 cagttactcc ttacgttcca caactatgat gattcgacct ttagattttt gaaagcgcaa 1320  
 tgtcagaagc gattatgaaa gcaacaaaga aatccggaga agctgccagg tgagaaactg 1380  
 tttgaaaact tcagaagcaa acaatattgt ctcccttcca gcaataagtg gtatgttatgt 1440  
 gaagtccacca aggttcttgc ccgtgaatct ggagccgtt gaggatcaca gagtcttac 1500

ttggggtgac agtgctcacg tggctcgact atagaaaaact ccactgactg tcgggctta	1560
aaaagggaaag aaactgctga gcttgctgtg cttcaaacta ctactggacc ttatttgga	1620
actatggtag ccagatgata aatatggta atttcatgta aaacagaaaa aaagagtcaa	1680
aaagagaata tacatgaaga atagaaaacaa gcctgccata atccttgga aaagatgtat	1740
tataccagtg aaaaggcggtt atatctatgc aaacctacta acaaattata ctgtgcaca	1800
atttgataa aaatttagaa cagcattgtc ctctgagttg gttaaatgtt aatggatttc	1860
agaaggctaa ttccagtatc atacttacta gttgatttct gcttacccat cttcaaatga	1920
aaattccatt tttgtaagcc ataatgaact gtagtacatg gacaataagt gtgtggtaga	1980
aacaaactcc attactctga ttttgatac agtttcaga aaaagaaaatg aacataatca	2040
agtaaggatg tatgtggtga aaacttacca cccccatact atggtttca tttactctaa	2100
aaactgattg aatgatatat aaatatattt atagcctgag taaagttaaa agaatgtaaa	2160
atatatcatc aagttcttaa aataatatac atgcatttaa tatttcctt gatattatac	2220
aggaaagcaa tattttggag tatgttaagt tgaagtaaaa ccaagtactc tggagcagtt	2280
cattttacag tatctacttg catgtgtata catacatgta acttcattat tttaaaaata	2340
tttttagaac tccaataactc accctgttat gtcttgctaa tttaaatttt gctaattaac	2400
tgaaacatgc ttaccagatt cacactgttc cagtgctat aaaagaaaca ctttgaagtc	2460
tataaaaaat aaaataattha taaatatcat tgtacatagc atgtttatat ctgcaaaaaaa	2520
cctaatacg aattaatctg gaatatgcaa cattgtcctt aattgatgca aataacacaa	2580
atgctcaaag aaatctacta tatcccttaa tgaaatacat cattcttcat atatttctcc	2640
ttcagtcctt tcccttaggc aatttttaat tttaaaaat tattatcagg ggagaaaaat	2700
tggcaaaaact attatatgta agggatatat atatacaaaa agaaaattaa tcatagtcac	2760
ctgactaaga aattctgact gctagttgcc ataaataact caatggaaat attcctatgg	2820
gataatgtat tttaagtgaa tttttgggt gcttgaagtt actgcattat tttatcaaga	2880
agtcttcctt gcctgttaagt gtccaaagggtt atgacagttaa acagttttta ttaaaacatg	2940
agtcaactatg ggtatgagaaa attgaaataa agctactggg cctcctctca taaaagagac	3000
agttgttggc aaggttagcaa taccagttc aaacttggtg acttgatcca ctatgcctta	3060
atgggttcctt ccatttgaga aaataaagct attcacattt ttaagaaaaa tacttttaa	3120
agtttaccat caagtctttt ttatattt gtgtctgtat tctacccctt tttgccttac	3180
aagtgtatatt tgcaggtatt ataccatttt tctattctt gtggcttctt catagcaggt	3240

aagcctctcc ttctaaaaac ttctcaactg ttttcattha	aggaaaagaa aatgagttt	3300
ttgtcctttt gtgtccctac agacacttac ttAAaccagt	ttttggataa agaataactat	3360
ttccaaactc atattacaaa aacaaaataa aataataaaa	aaagaaaagca tgatatttac	3420
tgtttgttg tctgggttg agaaaatgaaa tattgttcc	aattatttt aataaaatcag	3480
tataaaatgt tttatgattt ttagtgttat tatgtaatac	gtacatgttt atggcaattt	3540
aacatgtgta ttctttcat ttaattgttt cagaatagga	taatttaggtt ttcgaatttt	3600
gtctttaaaa ttcatgtggt ttctatgcaa agttcttcat	atcatcacaa cattatttga	3660
tttaaataaa attgaaatgt caccatggc agaaggagga	gggcagaatc atcacgaagt	3720
ggtgaagttc atggatgtct atcagcgcag ctactgccat	ccaatcgaga ccctggtgga	3780
catctccag gagtaccctg atgagatcga gtacatttc	aagccatcct gtgtccccct	3840
gatgcgatgc gggggctgct gcaatgacga gggcctggag	tgtgtgcccct ctgaggagtc	3900
caacatcacc atgcagatca tgcggatcaa acctcacca	ggccagcaca taggagagat	3960
gagcttccta cagcacaaca aatgtgaatg cagaccaaag	aaagatagag caagacaaga	4020
aaaatgtgac aagccgagggc ggtga		4045

&lt;210&gt; 122

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; ()..()

&lt;223&gt; Synthetic

&lt;400&gt; 122

Met	Trp	Gln	Ile	Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala
1				5				10					15		

Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys
					20			25					30		

Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro
					35			40					45		

Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Pro	Tyr	Val	Ser	Asn	Ala
					50			55				60		

Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val	Gln	Arg	Leu
					65			70			75		80		

Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp	Leu	Met	Lys
					85			90				95			

Val	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met	Val	Glu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100	105	110
Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly		
115	120	125
Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp		
130	135	140
Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu		
145	150	155
Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp		
165	170	175
Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu		
180	185	190
Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser		
195	200	205
Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn		
210	215	220
Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn		
225	230	235
Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn		
245	250	255
Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr		
260	265	270
Val Ala Lys Glu Glu Gln Ile Ser		
275	280	
<210> 123		
<211> 221		
<212> PRT		
<213> Homo sapiens		
<400> 123		
Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly		
1	5	10
15		
Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu		
20	25	30
Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Trp Thr		
35	40	45
Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp		
50	55	60
Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu		
65	70	75
80		
Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu		
85	90	95

Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr  
 100 105 110

Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu  
 115 120 125

Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His  
 130 135 140

Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys  
 145 150 155 160

Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly  
 165 170 175

Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly  
 180 185 190

Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser  
 195 200 205

Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe  
 210 215 220

<210> 124  
 <211> 1506  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 124  
 atgtggcaga ttgtttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60  
 aacttcgga agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc 120  
 tgcagctaca ctttcctcct gccagagatg gacaactgcc gctttcctc cagcccctac 180  
 gtgtccaatg ctgtgcagag ggacgcgccc ctcgaatacg atgactcggt gcagaggctg 240  
 caagtgcgtgg agaacatcat ggaaaacaac actcagtgcc taatgaaggt agagaatata 300  
 tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag 360  
 acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420  
 aagtttaactg atgtggaaagc ccaagtatta aatcagacca cgagacttga acttcagctc 480  
 ttggaacact ccctctcgac aaacaaattg gaaaaacaga ttttggacca gaccagtgaa 540  
 ataaacaaat tgcaagataa gaacagtttc ctagaaaaaga aggtgcttagc tatggaaagac 600  
 aagcacatca tccaactaca gtcaataaaa gaagagaaag atcagctaca ggtgttagta 660  
 tccaaggcaga attccatcat tgaagaactc gaaaaaaaaa tagtgactgc cacggtaat 720

aattcagttc ttcagaagca gcaacatgat ctcatggaga cagttataa cttactgact 780  
 atgatgtcca catcaaacgc agctaaggac cccactgttg ctaaagaaga acaaatcagc 840  
 gaggaagaga aaccatttag agactgtgca gatgtatatc aagctggttt taataaaagt 900  
 ggaatctaca ctattnatata taataatatg ccagaaccca aaaaggtgtt ttgcaatatg 960  
 gatgtcaatg ggggaggttg gactgtataa caacatcgtg aagatggaag tctagatttc 1020  
 caaaggact ggaaggaata taaaatgggt tttggaaatc cctccggta atattggctg 1080  
 gggaaatgagt ttattnnac cattaccagt cagaggcagt acatgctaag aattgagtt 1140  
 atggactggg aagggAACCG agccttattca cagttatgaca gattccacat aggaaatgaa 1200  
 aagcaaaact ataggttgta tttaaaaggt cacactggga cagcaggaaa acagagcagc 1260  
 ctgatcttac acggtgctga ttccagcact aaagatgctg ataatgacaa ctgtatgtgc 1320  
 aaatgtgccc tcatgttaac aggaggatgg tggtttcatg cttgtggccc ctccaaatcta 1380  
 aatggaaatgt tctataactgc gggacaaaac catggaaaac tgaatggat aaagtggcac 1440  
 tacttcaaag ggcccagtta ctccttacgt tccacaacta tgatgattcg accttttagat 1500  
 ttttga 1506

&lt;210&gt; 125

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; ()..()

&lt;223&gt; Synthetic

&lt;400&gt; 125

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala  
 1 5 10 15

Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys  
 20 25 30

Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro  
 35 40 45

Glu Met Asp Asn Cys Arg Ser Ser Ser Pro Tyr Val Ser Asn Ala  
 50 55 60

Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu  
 65 70 75 80

Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys  
 85 90 95

Val Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile  
 100 105 110  
 Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly  
 115 120 125  
 Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp  
 130 135 140  
 Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu  
 145 150 155 160  
 Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp  
 165 170 175  
 Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu  
 180 185 190  
 Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser  
 195 200 205  
 Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn  
 210 215 220  
 Ser Ile Ile Glu Glu Leu Glu Lys Ile Val Thr Ala Thr Val Asn  
 225 230 235 240  
 Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn  
 245 250 255  
 Asn Leu Leu Thr Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr  
 260 265 270  
 Val Ala Lys Glu Glu Gln Ile Ser Glu Glu Lys Pro Phe Arg Asp  
 275 280 285  
 Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr  
 290 295 300  
 Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met  
 305 310 315 320  
 Asp Val Asn Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly  
 325 330 335  
 Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly  
 340 345 350  
 Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile  
 355 360 365  
 Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu  
 370 375 380  
 Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu  
 385 390 395 400  
 Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly  
 405 410 415

Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp  
420 425 430

Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly  
435 440 445

Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe  
450 455 460

Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His  
465 470 475 480

Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile  
485 490 495

Arg Pro Leu Asp Phe  
500

<210> 126

<211> 648

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Synthetic

<400> 126

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
130 135 140

Pro Arg Arg Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu

145	150	155	160													
Val	Leu	Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile		
				165				170						175		
Gly	Lys	Lys	Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	
				180				185						190		
Leu	Leu	Pro	Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Pro	Tyr	Val		
				195			200						205			
Ser	Asn	Ala	Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val	
				210			215						220			
Gln	Arg	Leu	Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp	
				225			230			235				240		
Leu	Met	Lys	Val	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met	
				245				250						255		
Val	Glu	Ile	Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile	
				260				265						270		
Glu	Ile	Gly	Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys	
				275				280						285		
Leu	Thr	Asp	Val	Glu	Ala	Gln	Val	Leu	Asn	Gln	Thr	Thr	Arg	Leu	Glu	
				290				295						300		
Leu	Gln	Leu	Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln	
				305			310			315				320		
Ile	Leu	Asp	Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser	
				325				330						335		
Phe	Leu	Glu	Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln	
				340				345						350		
Leu	Gln	Ser	Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser	
				355				360						365		
Lys	Gln	Asn	Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala	
				370			375							380		
Thr	Val	Asn	Asn	Ser	Val	Leu	Gln	Gln	His	Asp	Leu	Met	Glu			
				385			390			395				400		
Thr	Val	Asn	Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Ala	Ala	Lys	
				405				410						415		
Asp	Pro	Thr	Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Glu	Glu	Lys	Pro		
				420				425						430		
Phe	Arg	Asp	Cys	Ala	Asp	Val	Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly	
				435				440						445		
Ile	Tyr	Thr	Ile	Tyr	Ile	Asn	Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe	
				450				455						460		

Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg  
465 470 475 480

Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met  
485 490 495

Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile  
500 505 510

Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met  
515 520 525

Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile  
530 535 540

Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly  
545 550 555 560

Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser  
565 570 575

Thr Lys Asp Ala Asp Asn Asn Cys Met Cys Lys Cys Ala Leu Met  
580 585 590

Leu Thr Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn  
595 600 605

Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile  
610 615 620

Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr  
625 630 635 640

Met Met Ile Arg Pro Leu Asp Phe  
645